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=> s methylat? (11a) cpg
L1 9438 METHYLAT? (11A) CPG

=> s l1 and (mass (3a) spectrom? or maldi)
L2 74 L1 AND (MASS (3A) SPECTROM? OR MALDI)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 40 DUP REM L2 (34 DUPLICATES REMOVED)

=> d 1-40 ti

L3 ANSWER 1 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Use of quantitative methylation-specific PCR of tumor suppressor gene promoters for detection of cervical cancer

L3 ANSWER 2 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Bisulfite-based assay of cytosine methylation status in gene promoter regions for improved diagnosis and treatment of breast cell proliferative disorders

L3 ANSWER 3 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methods for analyzing methylation patterns and polymorphisms in the DD3 gene promoter region associated with prostate cancer and methods for diagnosis

L3 ANSWER 4 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Detection of differential **CpG** dinucleotide **methylation** of genomic DNA for the analysis of colorectal cell proliferative disorders

L3 ANSWER 5 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Analysis of methylation status of calcitonin gene associated with cancer and methods for diagnosis and treatment

L3 ANSWER 6 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Analysis of **CpG** dinucleotide **methylation** status of human calcitonin gene associated with cancer

L3 ANSWER 7 OF 40 MEDLINE on STN DUPLICATE 1
TI A molecular understanding of mitoxantrone-DNA adduct formation: effect of cytosine methylation and flanking sequences.

L3 ANSWER 8 OF 40 MEDLINE on STN DUPLICATE 2
TI Rapid analysis of **CpG methylation** patterns using RNase T1 cleavage and **MALDI**-TOF.

L3 ANSWER 9 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methods and kits for detecting methylated nucleic acids

L3 ANSWER 10 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Method for the analysis of DNA methylation patterns by means of **mass spectrometry**

L3 ANSWER 11 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Identification of **methylated CpG** sequences in genomic DNA using 5-methylcytosine DNA glycosylase and related gene discovery and diagnostic methods

L3 ANSWER 12 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methods for detecting epigenetically silenced tumor suppressor genes and uses in human cancer diagnosis and therapy

L3 ANSWER 13 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methods for the analysis of cytosine methylation patterns in DNA and their diagnostic and prognostic applications

L3 ANSWER 14 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Method and nucleic acids for analysis of gene methylation status and single nucleotide polymorphisms associated with a lymphoid cell proliferative disorder

L3 ANSWER 15 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Diagnosis of colon cancer by bisulfite modification of human genomic DNA and PCR amplification of colon cancer-associated genes

L3 ANSWER 16 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI DNA- or PNA-array for detecting methylation within gene Melastatin for diagnosis of dermal cell proliferative disorders

L3 ANSWER 17 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methylation state analysis of genomic nucleic acids expressed in a colon cell proliferative disorders and their diagnostic and therapeutic uses

L3 ANSWER 18 OF 40 MEDLINE on STN DUPLICATE 3
TI Independent generation of 5-(2'-deoxycytidinyl)methyl radical and the formation of a novel cross-link lesion between 5-methylcytosine and guanine.

L3 ANSWER 19 OF 40 MEDLINE on STN DUPLICATE 4
TI Analysis and accurate quantification of **CpG methylation** by **MALDI mass spectrometry**.

L3 ANSWER 20 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5
TI Determining the degree of methylation of defined cytosines in genomic DNA in the sequence context 5'-CpG-3' by bisulfite modification

L3 ANSWER 21 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 6
TI Diagnosis and therapy of diseases by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 22 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 7
TI Diagnosis of diseases associated with cell signaling by detection of cytosine methylation in chemically modified genomic DNA

L3 ANSWER 23 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 8

TI Diagnosis and therapy of diseases associated with development genes by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 24 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 9
TI Diagnosis and therapy of diseases associated with signal transduction by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 25 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Methylation-silenced SOCS-1, SOCS-2, SOSC-3 and CIS-2 gene expression associated with cancer and their use in diagnosis and treatment

L3 ANSWER 26 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Analysis of human hematopoietic cell proliferative disorders by gene expression profiles and methylation status

L3 ANSWER 27 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Diagnosis and therapy of diseases associated with angiogenesis by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 28 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Oligonucleotides and method for determining methylation status of cdk4 gene and diagnosis of cancer

L3 ANSWER 29 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Oligonucleotides and methods for determining human c-mos gene methylation status and diagnosis of cancer

L3 ANSWER 30 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Method of detecting **methylated** cytosines in **CpG** islands of polynucleotides using **mass spectrometry** analysis for diagnosis and treatment of cancer

L3 ANSWER 31 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Using chemically modified DNA to detect cytosine methylation and single nucleotide polymorphisms in genes associated with cancer, behavioral and neurological diseases

L3 ANSWER 32 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Diagnosis and therapy of astrocytomas by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 33 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Diagnosis and therapy of genes associated with pharmacogenomics by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 34 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Detection of single nucleotide polymorphism and cytosine methylation in genes associated with differentiation of astrocytoma, oligoastrocytoma, and oligodendroglioma tumor cells using chemically modified genomic DNA

L3 ANSWER 35 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 10
TI Diagnosis and therapy of diseases associated with DNA repair by detection of single nucleotide polymorphism and cytosine methylation in chemically modified genomic DNA

L3 ANSWER 36 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Detection of single nucleotide polymorphisms and cytosine methylations in chemically modified genomic DNA for diagnosis and prognosis of genetic disorders

L3 ANSWER 37 OF 40 MEDLINE on STN DUPLICATE 11
TI A link between DNA methylation and epigenetic silencing in transgenic Volvox carteri.

L3 ANSWER 38 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Method for producing complex DNA methylation fingerprints

L3 ANSWER 39 OF 40 MEDLINE on STN DUPLICATE 12
TI Genome **methylation** of the marine annelid worm Chaetopterus variopedatus: **methylation** of a **CpG** in an expressed H1 histone gene.

L3 ANSWER 40 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
TI Hemoglobin Ozieri: a new α-chain variant (α71(E20)Ala→Val). Characterization using FAB- and electrospray-**mass spectrometric** techniques

=> d 19, 20, 30 bib ab

L3 ANSWER 19 OF 40 MEDLINE on STN DUPLICATE 4
AN 2003192960 MEDLINE
DN PubMed ID: 12711695
TI Analysis and accurate quantification of **CpG methylation** by **MALDI mass spectrometry**.
AU Tost Jorg; Schatz Philipp; Schuster Matthias; Berlin Kurt; Gut Ivo Glynne
CS Centre National de Genotypage, Batiment G2, 2 Rue Gaston Cremieux, CP 5721, 91057 Evry Cedex, France.
SO Nucleic acids research, (2003 May 1) 31 (9) e50.
Journal code: 0411011. ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200305
ED Entered STN: 20030425
Last Updated on STN: 20030520
Entered Medline: 20030519
AB As the DNA sequence of the human genome is now nearly finished, the main task of genome research is to elucidate gene function and regulation. DNA methylation is of particular importance for gene regulation and is strongly implicated in the development of cancer. Even minor changes in the degree of methylation can have severe consequences. An accurate quantification of the methylation status at any given position of the genome is a powerful diagnostic indicator. Here we present the first assay for the analysis and precise quantification of **methylation** on **CpG** positions in simplex and multiplex reactions based on matrix-assisted laser desorption/ ionisation **mass spectrometry** detection. Calibration curves for CpGs in two genes were established and an algorithm was developed to account for systematic fluctuations. Regression analysis gave R(2) >or= 0.99 and standard deviation around 2% for the different positions. The limit of detection was approximately 5% for the minor isomer. Calibrations showed no significant differences when carried out as simplex or multiplex analyses. All variable parameters were thoroughly investigated, several paraffin-embedded tissue biopsies were analysed and results were verified by established methods like analysis of cloned material. **Mass spectrometric** results were also compared to chip hybridisation.

L3 ANSWER 20 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 5
AN 2002:207192 CAPLUS
DN 137:28975

TI Determining the degree of methylation of defined cytosines in genomic DNA in the sequence context 5'-CpG-3' by bisulfite modification

IN Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt; Guetig, David

PA Epigenomics Ag, Germany

SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2

DT Patent

LA German

FAN.CNT 68

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002018632	A2	20020307	WO 2001-XI10074	20010901
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	DE 10044543	A1	20020404	DE 2000-10044543	20000905
	DE 10044543	C2	20030911		
	EP 1274865	A2	20030115	EP 2001-953936	20010406
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	JP 2003531589	T2	20031028	JP 2001-575634	20010406
	EP 1360319	A2	20031112	EP 2001-955278	20010406
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	DE 20121966	U1	20031224	DE 2001-20121966	20010702
	WO 2002018632	A2	20020307	WO 2001-EP10074	20010901
	WO 2002018632	A3	20040205		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2004067491	A1	20040408	US 2003-240454	20030311
	US 2003162194	A1	20030828	US 2003-240452	20030414
	JP 2004008217	A2	20040115	JP 2003-160375	20030605
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PRAI	DE 2000-10043826	A	20000901		
	DE 2000-10044543	A	20000905		
	WO 2001-EP10074	W	20010901		
	DE 2000-10019058	A	20000406		
	DE 2000-10019173	A	20000407		
	DE 2000-10032529	A	20000630		
	WO 2001-EP3969	W	20010406		
	WO 2001-EP4016	W	20010406		
	EP 2001-967115	A	20010702		
	EP 2002-90203	A	20020605		

AB The invention relates to a method for detecting the degree of methylation of a defined cytosine in the sequence context 5'-CpG-3' of a genomic DNA sample. The first stage involves treating the genomic DNA with bisulfite and subsequence alkaline hydrolysis in such a ways that the cytosine bases, but not the 5-methylcytosine bases, are converted into uracil, which corresponds to thymidine in its base pairing behavior. Parts of the

genomic DNA containing the defined cytosine are then amplified. The amplified parts are given a detectable mark and the extent of the hybridization of the amplified parts on the two classes of oligonucleotides is then determined by detecting the mark of the amplified parts. The degree of methylation of the defined cytosine in the genomic DNA sample can be deduced on the basis of the relationship between the marks detected on the two classes of oligonucleotides following the hybridization. The oligomer probes according to the present invention, containing at least one CpG dinucleotide, constitute important and effective tools which make it possible to ascertain the genetic and epigenetic parameters of genes associated with diseases. The invention is exemplified by methylation anal. of human genes ELK1 and MLH1. [This abstract record is one of ten records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L3 ANSWER 30 OF 40 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2002:51684 CAPLUS
DN 136:65187
TI Method of detecting **methylated** cytosines in **CpG** islands of polynucleotides using **mass spectrometry** analysis for diagnosis and treatment of cancer
IN Reich, Norbert O.; Wodtke, Alec M.
PA Epigenx Pharmaceutical, Inc., USA
SO PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002004686	A2	20020117	WO 2001-US41321	20010710
WO 2002004686	A3	20030918		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 2000-217059P	P	20000710	
US 2001-259559P	P	20010102	

AB The methylation status of cytosine bases in a polynucleotide can be determined, with enhanced sensitivity, by contacting the polynucleotide with an agent that modifies either unmethylated cytosine or methylated cytosine, amplifying the modified polynucleotide using one or more "heavyweight" nucleotides and then determining the mass of the amplified product. The polynucleotide is treated with a bisulfite salt which converts unmethylated cytosine to uracil. PCR is used to first generate a double stranded amplification product using a pair of natural primers to create a template for subsequent asym. amplification. Asym. PCR amplifies a single strand of the modified polynucleotide using adenine or thymine-containing heavyweight nucleotides that are halogenated with either bromine or iodine. Asym. amplification is achieved by adding an excess of one of the primers and by choosing an annealing temperature that favors annealing of one of the two primers. The mass of the amplified product is determined, for example, by **mass spectrometry**, and gauged in relation to the mass of a control sample having identical base sequence to the nucleotide sequence under study. A fully methylated or fully unmethylated control sample is used as the mass of the control sample can be estimated by mass of

the heavyweight and normal nucleotides. **Mass spectrometry** (Matrix Assisted Laser Desorption/Ionization or Electrospray **Mass spectrometry**) is conducted on a single strand of the double stranded amplification product with a primer chemical modified by addition of a water-soluble C60 derivative The presence or absence of a mass difference indicates whether one or more cytosine bases of the polynucleotide are methylated. The **methylation** of cytosine bases in **CpG** sequence motifs can be determined using this method which has implications in the diagnosis and treatment of cancer.